In the Specification

Page 1, after the Title and before line 4, insert the following new heading and paragraph:

-Cross-Reference To Related Application

This application is a continuation of U.S. application Serial No. 09/490,521, filed January 25, 2000 which claims the benefit of provisional application Serial No. 60/117,555, filed January 28, 1999.--

Replace the following paragraphs:

Page 10, lines 23 to 27 replace the paragraph with the following rewritten paragraph:

--It was possible to purify XG FTase 1400-fold by the end of the size exclusion chromatography step resulting in a total of 0.05 mg protein containing 70 nKat XG FTase activity. After biochemical purification and subsequent assay analysis, two polypeptides of approximately 65 kDa and 60 kDa in size were observed to co-purify repeatedly with XG FTase activity ~~(Figure 1)~~.--

Page 11, lines 12 to 15:

--Peptides from the lower molecular weight protein were not significantly similar to proteins of known function in databases, but did allow the identification of an Arabidopsis EST which, when translated contains four out of six peptides with amino acid identity ranging from 63%-85% ~~(See Table 2)~~.--

Page 11, lines 20 to 29:

--191A6T7 was used as a probe to screen the CD4-15 portion of a size-fractionated Arabidopsis cDNA library at high stringency (J - J - Kieber, M. Rothenberg, G. Roman, K. A. Feldmann, J. R. Ecker, *Cell* **72**, 427 (1993). Two cDNA clones were isolated, the longest containing a 1768 bp insert. Both lacked 13 nucleotides of the 3' UTR and the poly-A tail found in 191A6T7. There is an AATAAA consensus polyadenylation signal eight nucleotides from the 3' end of the library-derived clones. The sequence contains a 1698 nucleotide ORF that encodes a 63.7 kDa protein a 1698 nt open reading frame ~~(Table 3)~~ and correspond to a region of the fully sequenced Arabidopsis bacterial artificial chromosome (BAC) T18E14 ~~(Table 4)~~.--

Page 11, line 30 to page 12, 3:

--The cDNA and corresponding genomic clone have been designated AtFT1. Interestingly, analysis of the BAC indicates that there may be a second FTase approximately 600 bp downstream from AtFT1 which is ~60% identical to AtFT1 ~~(Table 5)~~. Whether this second FTase is expressed, as well as splicing patterns and localization of the encoded protein, are matters of current investigation. It does raise the possibility that a multi-gene family of FTases may exist in Arabidopsis. We will determine whether members of such a family might be differentially regulated by such

factors as environmental stress, tissue localization, or developmental stage. Alternatively, there may well be FTases which have different acceptors, such as carbohydrate protein modifications.--

Page 14, lines 6 to 10:

--AtFT1 is not significantly similar to any other FTases from other organisms, although multiple sequence alignments have identified three motifs which appear to be conserved among all alpha 1,2-FTases. One ([IV]G[IV]HQ][VI]R..[DN]; SEQ ID NO: 16) has been described previously (Breton et al., 1998). In addition, a second motif (D[EK]..F.[EQ].DQ; SEQ ID NO: 17) and a third hydrophobic region was conserved.--

Page 14, lines 21 to 26:

--The unique nature of this FTase allow its use as a tool for identifying other glycosyltransferases. Consideration of the number of different linkages present in plant cell wall polysaccharides indicates that there should be several hundred different glycosyltransferases involved in cell wall biosynthesis. Several other sequences in the Arabidopsis databases do appear to be similar to AtFT1 and AtFT2 and thus might represent a multi-gene family of FTases or glycosyltransferases. ~~Substantially identical sequences are presented in Tables 6-14~~.--